

```

RESULT 1
LOCUS      BE741672
DEFINITION BE741672          903 bp      mRNA linear      EST_15-SEP-2000
601594724.F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3948893 5',
ACCESSION  BE741672
VERSION     BE741672.1  GI:10155664
KEYWORDS    EST.

SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1 (bases 1 to 903)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: DCTD/DTP
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Sequencing Arrayed by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LHCMB12 row: 0 column: 06
            High quality sequence stop: 722.
            Location/Qualifiers

FEATURES
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                        /organism="Homo sapiens"

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/dh_xref="taxon:9606"
/clone="IMAGE:3948893"
/clone_lib="NH_MCC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="organ: ovary; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACTAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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[illegible]

D<sub>b</sub> 780 TGGCCACCTCAAACTCCCGAAGAACTGCTTCCGAGAAATATTCCTACCTTGAACATTAGG 839

O<sub>y</sub> 1264 GAAGAGCTCATTTTTTGTACATTTGTGTTAAAGAAAGACAAAACCTGAAC 1315

D<sub>b</sub> 840 GAGAGGCGCTTATTTGGAGCCTGGGGTCTTAAAGAGACAAAATGACCAAAATC 891

RESULT	2
BE271316	
LOCUS	628 bp mRNA linear EST 26-OCT-2000
DEFINITION	60114002.FP1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3049468 5',
ACCSSION	BE271316 mRNA sequence.
VERSION	BE271316
KEYWORDS	BE271316.1 GI:9144976 .EST.

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo. 1 (bases 1 to 628)
REFERENCE TITLE	NH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL COMMENT	Contact: Robert Strausberg, Ph. D.

cdna library Preparation: Ling Hong/Rubin Laboratory  
cdna library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
plates: LNC93 row: k column: 05  
High quality sequence crop: 628.  
Location/Qualifiers

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/clone="IMAGE:3049468"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(5). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT
174 a 170 c 172 g 112 t

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QY	807	CTTAGTGGAGACAGACACCTTCGGTAGTCAAGTCGGATCAAGGGCAAGGACGGAATT			866
Db	1	CCCTAGTGGAGACACACACCTTCGGTAGTCAAGTCGGATCAAGGGCAAGGACGGAATT			60
QY	867	CTACCTGTCATGAAACCGCAAGGCAAGCTCTGTGGGGAAGGCCGANTGGCACCAGCAAGCA			926
Db	61	CTACCTGTGCTAGTAACCGCAAGGCAAGCTCTGTGGGGAAGGCCGANTGGCACCAGCAAGCA			120
QY	927	GTGTGTTTCATCAGAGAAGTTCTGAGAAACATACACGCGCCCTGATGTGCGCTAAAGTA			986
Db	121	GTGTGTTTCATCAGAGAAGTTCTGAGAAACATACACGCGCCCTGATGTGCGCTAAAGTA			180
QY	987	CTCCGGCTGGTACGTGGGCTTACCAAGABAGGGCGCGCCGGGAAGGGCCCCCAAGACCCG			1046
Db	181	CTCCGGCTGGTACGTGGGCTTACCAAGABAGGGCGCGCCGGGAAGGGCCCCCAAGACCCG			240

QY 1047 GGAGACCAGCAGGACGTCATTCATGACGCGTACCCAGGAGGAGCCGAGCTTCA 1106  
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 Db 241 GGAGACACGACGACGTCATTCATGACGCGTACCCAGGAGGAGCCGAGCTTCA 300  
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 QY 1107 GAAGCCCTTCAAGTACACGACGCGTACCCAGGAGGAGCCGAGCTTCA 1166  
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 Db 301 GAAGCCCTTCAAGTACACGACGCGTACCCAGGAGGAGCCGAGCTTCA 360  
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 QY 1167 TGCCCTAGGACACCCCGCGGCGCCCTCAGTCCGCTGCGACACTCACCAGAA 1226  
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 Db 361 TGCCCTAGGACACCCCGCGGCGCCCTCAGTCCGCTGCGACACTCACCAGAA 420  
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 QY 1227 AACTGCATCAGAGATATTTTACATGATAAATAGGAGAGCTCTATTGTGACAT 1286  
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 Db 421 AACTGCATCAGAGATATTTTACATGATAAATAGGAGAGCTCTATTGTGACAT 480  
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 QY 1287 TGTGTTTAAAGAGACAAAACCTGAAACCAAACTCTTGCGGAGGAGGATATAA-GGAT 1345  
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 Db 481 TGTGTTTAAAGAGACAAAACCTGAAACCAAACTCTTGCGGAGGAGGATATAA 540  
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 QY 1346 TTTTATGTTGACTGAAACCCCGCATGACAAAGACTCAGCAAAAGGACTGTAGTCAAC 1405  
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 Db 541 CTTATGTTGACTGAAACCCCGCATGACAAAGACTCAGCAAAAGGACTGTAGTCAAC 600  
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 QY 1406 CCACAGGTGCTGTCTCTCTCTAGAAC 1433  
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 Db 601 CCACAGGTGCTGTCTCTCTCTAGAAC 628  
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 RESULT 3  
 BE315016 639 bp mRNA linear EST 26-OCT-2000  
 LOCUS 601140772F1 NIH\_MGC\_9 Homo sapiens CDNA clone IMAGE:3049984 5,  
 DEFINITION  
 mRNA sequence.  
 BE315016  
 VERSION BE315016.1 GI:9145233  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 639)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-femail.nih.gov  
 Tissue Procurement: DCTD/DRP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: L1CM94 row: P column: 17  
 High quality sequence stop: 637.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: ovary; Vector: pOTB; Site: 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 148 a 194 c 199 g 98 t  
 ORIGIN

Query Match 39.1%: Score 613.4; DB 10; Length 639;  
 Best Local Similarity 99.5%; Pred. No. 7.3e-74;  
 Matches 636; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
 QY 599 TGCCTGCTTCAGTACAGTGTGCTGCTGCC-GAGGAGAACGTGACTTCGCATCCAC 657  
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 QY 658 GTGAGAACACAGACGCGGGCTCGGAGCATGTGACCGCTAAGACCTCGGCTGATCAG 717  
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 Db 61 GTGAGAACACAGACGCGGGCTCGGAGCATGTGACCGCTAAGACCTCGGCTGATCAG 120  
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 QY 718 CTCTACACCGGACAGTGGGAAACACTCCAGGCTCGGGCCGAGGATGACGCGCCG 777  
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 Db 121 CTCTACACCGGACAGTGGGAAACACTCCAGGCTCGGGCCGAGGATGACGCGCCG 180  
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 QY 778 GCGGAGATGGGAGCAATGATGCTCCAGCTCTAGTGAAGACAGACCTTCGTAGTCAA 837  
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 Db 181 GCGGAGATGGGAGCAATGATGCTCCAGCTCTAGTGAAGACAGACCTTCGTAGTCAA 240  
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 QY 838 GTCCGATCAAGGCGCAAGAGCGAATTTACCTGTGATGAACCGCAAGGCAAGCTC 897  
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 Db 241 GTCCGATCAAGGCGCAAGAGCGAATTTACCTGTGATGAACCGCAAGGCAAGCTC 300  
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 Db 301 GTGGGGAAGCCCGATGGCAGCAGAGAGTGTGTTCATCAGAGAGTTCTGGAGAAC 360  
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 QY 1017 GGGGCGGCGCGGGAAGGCGCCCAAGACCCGGGAGAAACAGCAGAGCTGATTTGATGAA 1076  
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 Db 421 GGGGCGGCGCGGGAAGGCGCCCAAGACCCGGGAGAAACAGCAGAGCTGATTTGATGAA 480  
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 RESULT 4  
 A1743298 455 bp mRNA linear EST 20-DEC-1999  
 LOCUS wg91b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_S1 Homo sapiens CDNA clone  
 DEFINITION IMAGE:2372429 3' similar to TR:076093 076093 FIBROBLAST GROWTH  
 FACTOR 18. ; mRNA sequence.  
 A1743298  
 VERSION A1743298.1 GI:5111586  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 455)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-femail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert length: 561 Std Error: 0.00

Seq primer: -400P from Gibco.  
FEATURES  
source Location/Qualifiers  
1..455  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2372429"  
/clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneids: Soares NB2HP pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HPF-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 122 c 103 g 89 t  
ORIGIN

Query Match 28.9%; Score 453.4; DB 9; Length 455;  
Best Local Similarity 99.8%; Pred. No. 3.3e-52;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1075 AACGCTACCCCAAGGGGCGAGCGGAGCTTCACAAAGCCCTTCAGATACAGAGCGTGACC 1134  
DB 1 AAGCGTACCCCAAGGGGCGAGCGGAGCTTCAGATACAGAGCGTGACC 60

QY 1135 AAGAGTCCCGTGGATCCGCGCCACACACCCCTGCTAGGCGCCCGCGGGCCCTC 1194  
DB 61 AAGAGTCCCGTGGATCCGCGCCACACACCCCTGCTAGGCGCCCGCGGGCCCTC 120

QY 1195 AGGTGCCCCGCGACACTCACCCTCCAGAAAATGCATCAGAGAAATTTTTCATG 1254  
DB 121 AGGTGCCCCGCGACACTCACCCTCCAGAAAATGCATCAGAGAAATTTTTCATG 180

QY 1255 AAAAATTAAGGAGAACTCTATTGTTGTACATTTGTTTAAAGAGACAAAATCTGAAC 1314  
DB 181 AAAAATTAAGGAGAACTCTATTGTTGTACATTTGTTTAAAGAGACAAAATCTGAAC 240

QY 1315 CAAAACTCTGGGGGAGGGGATGAATTAAGATTTTATGTTGACTTGAACCCCGGATGAC 1374  
DB 241 CAAAACTCTGGGGGAGGGGATGAATTAAGATTTTATGTTGACTTGAACCCCGGATGAC 300

QY 1375 AAAAGACTCAGCAAGGAGCTGTAGTCAACCCACAGTGTCTCTCTCTAGAGACA 1434  
DB 301 AAAAGACTCAGCAAGGAGCTGTAGTCAACCCACAGTGTCTCTCTCTAGAGACA 360

QY 1435 GACAACTCTAACTCGTCCCGCAGAGAGACTTGAATGAGAAACCAACTTTGAGAAG 1494  
DB 361 GACAACTCTAACTCGTCCCGCAGAGAGACTTGAATGAGAAACCAACTTTGAGAAG 420

QY 1495 CCAAACTCTTTTCCCAAGGTTCTGANAAGAAA 1529  
DB 421 CCAAACTCTTTTCCCAAGGTTCTGANAAGAAA 455

RESULT 5  
LOCUS A1148578 449 bp mRNA linear EST 27-OCT-1998  
DEFINITION qc88a11.x1 Soares\_placenta\_8to9weeks\_2NBHP8to9w Homo sapiens cDNA  
clone IMAGE:1713788 3', mRNA sequence.  
ACCESSION A1148578  
VERSION A1148578.1 GI:3677047  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 449)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 538 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.  
Location/Qualifiers  
1..449  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1713788"  
/clone\_lib="Soares\_placenta\_8to9weeks\_2NBHP8to9w"  
/dev\_stage="two placenta: one from 8 weeks and another from 9 weeks post conception"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer (5' TGTTACCATCTGAAGTGGAGCGCGCGCGATTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and Eco RI and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 135 a 123 c 106 g 85 t  
ORIGIN

Query Match 28.6%; Score 449; DB 9; Length 449;  
Best Local Similarity 100.0%; Pred. No. 1.3e-51;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1040 AGACCCGGGAGAACACGACGACGTCATTTTCATGAAGCGCTACCCCAAGGGGCGACCGG 1099  
DB 1 AGACCCGGGAGAACACGACGACGTCATTTTCATGAAGCGCTACCCCAAGGGGCGACCGG 60

QY 1100 AGCTTGAGAGCCCTTCAAGTACAGCAGCGTGACCAAGAGTCCGTCGATCCGCCCA 1159  
DB 61 AGCTTGAGAGCCCTTCAAGTACAGCAGCGTGACCAAGAGTCCGTCGATCCGCCCA 120

QY 1160 CACACCTCGCTTAGGCGACCCCGCGCGCCCTCAGTGCCTGCGCACACTCAGCT 1219  
DB 121 CACACCTCGCTTAGGCGACCCCGCGCGCCCTCAGTGCCTGCGCACACTCAGCT 180

QY 1220 CCAGAAAATCTGCATCAGAGGAAATTTTATACATGAAAATTAAGAAAGAGTCTATTTT 1279  
DB 181 CCAGAAAATCTGCATCAGAGGAAATTTTATACATGAAAATTAAGAAAGAGTCTATTTT 240

QY 1280 TGTACATTTGTTTAAAGAGACAAAATCTGAACAAACTCTTGGGGGAGGGGTAT 1339  
DB 241 TGTACATTTGTTTAAAGAGACAAAATCTGAACAAACTCTTGGGGGAGGGGTAT 300

QY 1340 AAGGATTTTATTTGACTTGAACCCCGGATGACAAAAGACTCACGCAAGGACTGTA 1399  
DB 301 AAGGATTTTATTTGACTTGAACCCCGGATGACAAAAGACTCACGCAAGGACTGTA 360

QY 1400 GTCAACCCACAGGCTGTCTCTCTAGAGAACAGACAACTCTAACTCCGTCGCCACAG 1459  
DB 361 GTCAACCCACAGGCTGTCTCTCTCTAGAGAACAGACAACTCTAACTCCGTCGCCACAG 420

QY 1460 GAGGACTTGAATGAGAAACCAACTTT 1488  
DB 421 GAGGACTTGAATGAGAAACCAACTTT 449

RESULT 6

LOCUS	AM530232	515 bp	mRNA	Linear	EST 06-MAR-2000
DEFINITION	UT-R-BU0-amu-b-08-0-UI.s1 UT-R-BU0 Rattus norvegicus cDNA clone				
ACCESSION	AM530232				
VERSION	AM530232.1				
KEYWORDS	GI:7172646				
SOURCE	EST.				
ORGANISM	Norway rat. Rattus norvegicus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (Bases 1 to 515) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996) 9704477				
REFERENCE AUTHORS TITLE					
JOURNAL MEDLINE COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Oligo-dT trick not found, Not i site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 39-64, >CC-richlow_complexity Seq primer: M13 Forward POLYA-No.				

### FEATURES

#### Location/Qualifiers

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1..organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone_uri="R-800-amu-b-08-0-01"
/clone_lib="uri-R-B00"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker. Site:1: Not I; Site:2: Eco RI. The uri-R-B00
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratstat.eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
```

BASE COUNT	112 a	139 c	164 g
ORIGIN			

Query Match	27.98;	Score 437.4;	DB 10;	Length 515;
Post 10007	01.00;	Score 437.4; <td>DB 10;<td>Length 515;</td></td>	DB 10; <td>Length 515;</td>	Length 515;

Matches 473; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

487 CGGCCGCGGACATGTGCAGGCTGGGCTAGGAGCCGCCCT -CCCTCCGCC 545

Db 1 CGGCCGCGGAGCGACATGTGCAGGCTGGGCTAGGAGCCGCCCTCCCCCCCCGCC 60

546 AGCGATGATTACAGCGCCCTCCGCTGCACCTTGCCCTGTGTTACACTTCCTGCTGCTGTC 605

Db 61 CGCGATGATTCAGCGCCCTCCGCCCTGCACCTTGCCCTGTGTTACACTTCTACTGCTGTG 120

606 CTTCAGGTACAGGTGCTGGTTGCCGAGGAGAACGTGGACTTCCGCATCCACGTGGAGAA 665

Db 121 CTTCAGGTTCAAGTGTGGCAGCCGAGGAGAACGTGGACTTCCGCATCCATGTGGAGAA 180

666 CCAGACGGGGCTCGGACGATGTGAGCCGTAA GCAGCTGCGGCTGTACCAGCTCTACAG 725

Accession	Sequence	Position
Dp	CCAGACTTCGGGCTGCGCATGTATGTGAGTCGGAAACCACTGCGCTTGTACCAAGCTCTACAG	240
Qy	CCGAGCAGTGGGAAACACATCCAGGTCTCTGGGCGCGAGATCAGTACCCGCGCGAAGA	785
Dp	CAGAGCCAGTGGGAAGACATTCAAAGTCCTGGGCGCGTAGATCAGTCCCGTGGCGAAGA	300
Qy	TGGGGACAAGTATGCCAGCTCCCTAGTGGAGACAGACACTTCGGTATGTCAAGTCCGGAT	845
Dp	CGGGACAAGTATGCCAGCTCCCTAGTGGAGACAGACACTTCGGGAGTCAAGTCCGGAT	360
Qy	CAAGGCGAAGAGAGACGGAATTCCTCTGTGATCAATCCGCAAAAGCCAAAGCTCGTGGGAA	905
Dp	CAAGGCGAAGAGAGACAGAGTTCTTACCTCTGTATATCAACCGAAGAGCAAGCTCGTGGGAA	420
Qy	GCCCGATGGCACACGACGAAGAGTGTGTTATCATGACAGAAGTTCTGGAGAACCACTACAC	965
Dp	GCTGATGTGACTAGCAAGGAGTGCCTGTTCATGTGAGAAGTCTTGAAAACCAACTACAC	480
Qy	GGCCCTGATGTCGGCTAAAGTACTCCGCTGGTAGC	1000
Dp	GGCCCTGATGTCAGCAAGTACTAGGCTGGTAGC	515

Db 481 GGCCCTGATGTCAGCCAGTACTCAGGCTGGTACG 515

1  
1  
2  
1  
1  
1  
1  
3  
3

AI333518

DEFINITION qp96a07.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone .

ACCESSION AI333518  
VERSION AI333518 1 CT-4070077

**KEYWORDS** EST. **EST.**  
COUNTY **EST.**

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 4,326)

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute Cancer Genome Project

**Tumor Gene Index**  
Published (1987)

**COMMENT**  
Contact: Robert Strausberg, Ph.D.  
Email: [csaahb-r@mail.nih.gov](mailto:csaahb-r@mail.nih.gov)

This clone is available royalty-free through LNL ; contact the TWACE Consortium ([info@twace.nl](mailto:info@twace.nl)) for further information

Insert Length: 1051 Std Err

FEATURES	Location/Qualifiers
Source	1 436

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:1930836"  
/clone lib="Scars foto" lura nbu10w
```

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/dev_stage="19 weeks"
lab_host="nu10b.cmcjci111.cmcjci.com"
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```

/note="Organ: Lung; Vector: pT7T3D (Phar
modified polymer: site 1", not T", site

```

strand cDNA was primed with a Not I - oligo(dt) primer  
 15'-TGGTACCAATCTCAACTCGGACGGCGCCCAATTTTTTTTTTTTTTTTTT-

double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia) digested with Not I and cloned in

the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of

normalization to a  $Cot = 5$ . Library constructed by Ben Soares and M Fátima Bonaldó. This library was constructed

from the same fetus as the fetal heart library, Soares  
fatal heart NhhH19w "

BASE COUNT	133 a	120 c	9 / 9	86 f
ORIGIN				

Query Match 27 69: Score 432 8: DB 0: Length 436:

Best Local Similarity 99.58; Pred. No. 2e-49;  
Matches 434; Conservative 0; Mismatches 3; Indels 0;  
Gaps 0;

QY 1075 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAAAGCCCTTCAAGTACAGCGGTGACC 1134  
 DB 1 AAGGCTACCCCAAGGGGAGCCGAGCTTCAGAAAGCCCTTCAAGTACAGCGGTGACC 60  
 QY 1135 AAGAGTCCCGTGGGATCCGCGCCACACACCTTCTAGGCGACCCCGCGGCCCTC 1194  
 DB 61 AAGAGTCCCGTGGGATCCGCGCCACACACCTTCTAGGCGACCCCGCGGCCCTC 120  
 QY 1195 AGTCCGCTGGGACACTCACAATCCAGAAAACCTCATCAGAGATATTTTACATG 1254  
 DB 121 AGTCCGCTGGGACACTCACAATCCAGAAAACCTCATCAGAGATATTTTACATG 180  
 QY 1255 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACCTGAC 1314  
 DB 181 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACCTGAC 240  
 QY 1315 CAAACCTCTGGGGGAGGGGATAGAGATTTTATTTGTTGACTGTGAACCCCGATGAC 1374  
 DB 241 CAAACCTCTGGGGGAGGGGATAGAGATTTTATTTGTTGACTGTGAACCCCGATGAC 300  
 QY 1375 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTCTAGAGACA 1434  
 DB 301 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTCTAGAGACA 360  
 QY 1435 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAACCAACTTTGAGAG 1494  
 DB 361 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAACCAACTTTGAGAG 420  
 QY 1495 CCAAGCTCTTTTCC 1510  
 DB 421 CCAAGCTCTTTTCC 436  
 RESULT 8  
 A1621022 427 bp mRNA linear EST 21-APR-1999  
 LOCUS t57b11.x1 NCI-CGAP.GC6 Homo sapiens cDNA clone IMAGE:2237180 3'  
 DEFINITION similar to TR:076093 076093 FIBROBLAST GROWTH FACTOR 18. ;, mRNA  
 sequence.  
 ACCESSION A1621022  
 VERSION A1621022.1 GI:4630148  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 427)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgarbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bdrp/image/image.html](http://www.bio.llnl.gov/bdrp/image/image.html)  
 Seq primer: -400p from Gibco.  
 FEATURES  
 source  
 1. 427  
 location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2237180"  
 /clone\_1ib="NCI-CGAP.GC6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: p17T3D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP.GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 1257096-1258631, 146964-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 132 a 116 c 97 g 81 t 1 others  
 ORIGIN  
 Query Match 27.0%; Score 424.4; DB 9; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-48;  
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1075 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAAAGCCCTTCAAGTACAGCGGTGACC 1134  
 DB 1 AAGGCTACCCCAAGGGGAGCCGAGCTTCAGAAAGCCCTTCAAGTACAGCGGTGACC 60  
 QY 1135 AAGAGTCCCGTGGGATCCGCGCCACACACCTTCTAGGCGACCCCGCGGCCCTC 1194  
 DB 61 AAGAGTCCCGTGGGATCCGCGCCACACACCTTCTAGGCGACCCCGCGGCCCTC 120  
 QY 1195 AGTCCGCTGGGACACTCACAATCCAGAAAACCTCATCAGAGATATTTTACATG 1254  
 DB 121 AGTCCGCTGGGACACTCACAATCCAGAAAACCTCATCAGAGATATTTTACATG 180  
 QY 1255 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACCTGAC 1314  
 DB 181 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACCTGAC 240  
 QY 1315 CAAACCTCTGGGGGAGGGGATAGAGATTTTATTTGTTGACTGTGAACCCCGATGAC 1374  
 DB 241 CAAACCTCTGGGGGAGGGGATAGAGATTTTATTTGTTGACTGTGAACCCCGATGAC 300  
 QY 1375 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTCTAGAGACA 1434  
 DB 301 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTCTAGAGACA 360  
 QY 1435 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAACCAACTTTGAGAG 1494  
 DB 361 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAACCAACTTTGAGAG 420  
 QY 1495 CCAAGCTCTTTTCC 1501  
 DB 421 CCAAGCTCTTTTCC 427  
 RESULT 9  
 BF471928 617 bp mRNA linear EST 04-DEC-2000  
 LOCUS UI-M-BH3-awr-c-01-0-UI.r1 NIH.BMAP.M.S4 Mus musculus cDNA clone  
 DEFINITION UI-M-BH3-awr-c-01-0-UI 5', mRNA sequence.  
 ACCESSION BF471928  
 VERSION BF471928.1 GI:11541111  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 617)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 JOURNAL MEDLINE  
 97044477  
 COMMENT  
 Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd., Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mestr@mail.nih.gov





Matches 444: Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 1075 AAGCGTACCCCAAGGGGACCGGAGCTTCAGAGACCCCTTCAAGTACACGAGGTGACC 1134  
|||||  
Db 1 AAGCGTACCCCAAGGGGACCGGAGCTTCAGAGACCCCTTCAAGTACACGAGGTGACC 60  
|||||

QY 1135 AAGAGTCCCGTGGATCCGGCCACACACCTTGGCTTGGCCACCCCGCGGCCCTTC 1194  
|||||  
Db 61 AAGAGTCCCGTGGATCCGGCCACACACCTTGGCTTGGCCACCCCGCGGCCCTTC 120  
|||||

QY 1195 AGTTCGCCCTGGCCACACTCCACCTCCAGAAACCTGATCAGAGATATTTTACATG 1254  
|||||  
Db 121 AGTTCGCCCTGGCCACACTCCACCTCCAGAAACCTGATCAGAGATATTTTACATG 180  
|||||

QY 1255 AAAAATAAGAGAAGACTCTATTTTGTGATCTGTGTTAAAGACAAAACCTGATC 1314  
|||||  
Db 181 AAAAATAAGAGAAGACTCTATTTTGTGATCTGTGTTAAAGACAAAACCTGATC 240  
|||||

QY 1315 CAAACCTCTTGGGGGAGGGGTGATAGATTTATTTGATCTGAAACCCCGCA -TGA 1373  
|||||  
Db 241 CAAACCTCTTGGGGGAGGGGTGATAGATTTATTTGATCTGAAACCCCGATTTGA 300  
|||||

QY 1374 CAAAGACTCAG -GCAAGGAGCTGTAGTCAACCCACAGGTGC -TTGTCTCTCTAGGA 1431  
|||||  
Db 301 CAAAGACTCAGGCAAGGAGCTGTAGTCAACCCACAGGTGCTTGTCTCTCTAGGA 360  
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QY 1432 ACAGACACTCTTAACCTGTCTCCAGAGAGAGACTTGAATGAGAAACCAACTTTGAG 1491  
|||||  
Db 361 ACAGACACTCTTAACCTGTCTCCAGAGAGAGACTTGAATGAGAAACCAACTTTGAG 420  
|||||

QY 1492 AAGCCAAAGTCTTTTCCCAAGGTCT 1520  
|||||  
Db 421 AAGCCAAAGTCTTTTCCCAAGGTCT 449  
|||||

RESULT 11  
BF564483/c 517 bp mRNA linear EST 12-DEC-2000  
LOCUS UI-R-BU0-amu-b-08-0-UI.r1 UI-R-BU0 Rattus norvegicus cDNA clone  
DEFINITION UI-R-BU0-amu-b-08-0-UI.5, mRNA sequence.  
ACCESSION BF564483 GI:11674213  
VERSION BF564483  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 517)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL MEDLINE  
COMMENT 97044477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: mscares@blue.weeg.uiowa.edu  
cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
clones will be available through Research Genetics (www.resgen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
LNLN (info@image.llnl.gov). IMAGE ID= 1801316  
Seq primer: M13 Forward.  
FEATURES  
source  
1..517  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-BU0-amu-b-08-0-UI"  
/clone\_1lib="UI-R-BU0"

/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-pac (Pharmacia) with a modified  
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-BU0  
library is a subtracted library derived from a mixture of  
eye and ganglia tissues. For a detailed description of the  
library from which this clone was derived, please visit  
our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has  
been previously described in (Bonaldo, Lennon and Soares,  
Genome Research 6:791-806, 1996)" 1 others  
BASE COUNT 89 a 154 c 140 g 133 t  
ORIGIN  
Query Match 26.0%; Score 408; DB 12; Length 517;  
Best Local Similarity 88.7%; Pred. No. 4, 1e-46;  
Matches 441; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 680 GGGACATGTGAGCCCGTAACAGCTGGGCTGTACACGCTCTACAGCCGACAGTGGGA 739  
|||||  
Db 517 GCGATGATGTGAGTGGAGACAGCTGGCTGTGACAGCTCTACAGCAGCAGTGGGA 458  
|||||

QY 740 AACACATCCAGTCTGGGCGCGAGATCAGTCCGCGCGAGAGATGGGACAAATAG 739  
|||||  
Db 457 AGCAGATTCAGTCTGGGCGCGAGATCAGTCCGCGCGAGAGATGGGACAAATAG 398  
|||||

QY 800 CCCAGCTCTAGTGGAGACAGACACTTCGTAAGTCAAGTCCGATCAAGGCAAGAGA 859  
|||||  
Db 397 CCCAGCTCTAGTGGAGACAGACTTCGTAAGTCAAGTCCGATCAAGGCAAGAGA 338  
|||||

QY 860 CGGAATTCATCCCTGTGATGACAGCCGCAAGGCAAGCTGTGGGGAAGCCGATGACACA 919  
|||||  
Db 337 CAGAGTTTATCTGTGTATGATACCGAAAGGCTGTGGGGAAGCCGATGATCA 278  
|||||

QY 920 GCAAGAGTGTGTGTATCATGAGAGAGTCTGTGAGAACTACAGCGCCCTGATGCG 979  
|||||  
Db 277 GCAAGAGTGTGTGTATCATGAGAGAGTCTGTGAGAACTACAGCGCCCTGATGCG 218.  
|||||

QY 980 CTAAAGTACTCCGGCTGTGATGAGGCTTCAACCAAGAGGGGCGCGGAGAGGCCCA 1039  
|||||  
Db 217 CCAAGTACTCAGGCTGTGATGAGGCTTCAACCAAGAGGGGCGCGGAGAGGCCCA 158  
|||||

QY 1040 AGACCCGGGAGAACAGCAGAGAGTCAATTTATGAAAGGCTACACCAAGGGGCGCGG 1093  
|||||  
Db 157 AGACCCGGGAGAACAGCAGAGAGTCAATTTATGAAAGGCTACACCAAGGGGCGCGG 98  
|||||

QY 1100 AGCTTCAGAGAGCCCTTCAAGTACAGCAGCGGTGACCAAGAGTCCGCTGATCCGCCCA 1159  
|||||  
Db 97 AGCTTCAGAGAGCCCTTCAAGTACAGCAGCGGTGACCAAGAGTCCGCTGATCCGCCCA 38  
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QY 1160 CACACCTCTGCTAGGCC 1176  
|||||  
Db 37 CTCACCCCGCTAGGTC 21  
|||||

RESULT 12  
BG800960 600 bp mRNA linear EST 20-DEC-2001  
LOCUS 0081-34 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,  
DEFINITION mRNA sequence.  
ACCESSION BG800960 GI:17947827  
VERSION BG800960.1  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 600)  
Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,  
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Kleit, W.H.  
Gene expression in the developing mouse retina by EST sequencing  
and microarray analysis  
Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
JOURNAL MEDLINE  
21671825



## COMMENT

Contact: Klein WH  
Department of Biochemistry and Molecular Biology  
University of Texas M.D. Anderson Cancer Center  
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
Tel: 713 792 3646  
Fax: 713 790 0329.

## FEATURES

source  
Location/Qualifiers  
1. 600  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone\_1lb="Mouse E14.5 retina lambda ZAP II Library"  
/tissue\_type="neural retina"  
/dev\_stage="embryonic day 14.5 post-fertilization"  
/note="Vector: PAMP10 (Gibco): Cloned unidirectionally.  
Primer: Oligo dt. RNA Isolation: cytoplasmic RNA preps  
(Mammatils); Cloning Technique: CUA Cloning (cloneamp,  
Life Technologies); Average insert size: 1.8 Kb;  
Insertion site: TACGTCCACTGATTCGTAGT-->. Other  
information regarding entire library may be found at  
http://pga.swmed.edu/Data/Libraries/microarray\_cdna\_library.htm"

BASE COUNT 159 a 158 c 172 g 105 t 6 others  
ORIGIN

Query Match 25.8%; Score 404.6; DB 12; Length 600;  
Best Local Similarity 86.3%; Pred. No. 1.1e-45;  
Matches 491; Conservative 0; Mismatches 73; Indels 5; Gaps 4;

QY 629 CCGAGGAAAGTGGACTTCGCATCCATGGAACACAGCGGGCTGGGACGATG 688  
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Db 8 CCGAGGAGATGTGACATTCGCATCCATGGAACACAGCGGGCTGGGACGATG 67  
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QY 689 TGAAGCCTAAGCAGCTGGGCTGTACAGCTTACACCGGACCACTGGGAACACTTC 748  
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Db 68 TGAAGCCTAAGCAGCTGGGCTGTACAGCTTACACCGGACCACTGGGAACACTTC 127  
|||||

QY 749 AGGTCTGGGCGCAGAGTATGCGCGCGAGATGGGAGCAATATGCCAGCTCC 808  
|||||

Db 128 AAGTCTGGGCGCAGAGTATGCGCGCGAGATGGGAGCAATATGCCAGCTCC 187  
|||||

QY 809 TACTGAGACAGACACCTTGGTATCAATCCGATCAAGGGCAAGAGACGGAATTC 868  
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Db 188 TACTGAGACAGACACCTTGGTATCAATCCGATCAAGGGCAAGAGACGGAATTC 247  
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QY 869 ACCTGTCCATGAA-CCGCAAAAGCAGACTGTGGGGAAGCCGATGACACAGAGAG 927  
|||||

Db 248 ACCTGTCCATGAA-CCGCAAAAGCAGACTGTGGGGAAGCCGATGATAGCAAGAG 307  
|||||

QY 928 TGTGTGTTATCGAAGGTTCTGGAGAACACTACAGGCGCTGATGTGGCTAAGTAC 987  
|||||

Db 308 TGTGTGTTATCGAAGGTTCTGGAGAACACTACAGGCGCTGATGTGGCTAAGTAC 367  
|||||

QY 988 TCCGCTGTAGTGGGCTTACCAAGAGGGGCGCGGGAAGGGGCCCAAGACCCGG 1047  
|||||

Db 368 TCCGCTGTAGTGGGCTTACCAAGAGGGGCGCGGGAAGGGGCCCAAGACCCGG 427  
|||||

QY 1048 GAGACAGAGGAGCGGCTTTCATGAAGCGCTACCCCAAGGGGCGCGGAGCTTCAG 1107  
|||||

Db 428 GAGACAGAGGAGCGGCTTTCATGAAGCGCTACCCCAAGGGGCGCGGAGCTTCAG 486  
|||||

QY 1108 AAGCCCTTCAAGTACAGAGGTGACCAAGAGTCCCGTGATGCCGCGCACACACCT 1167  
|||||

Db 487 AA-CCCTTNAATACACACAGTACACCAAGCATCCMG--GGGATCCGCCACTTACCCC 543  
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QY 1168 GCCTAGGACACCCCGCGCGGCGGCTTCAG 1196  
|||||

Db 544 GGNTAGGTCCGCGACACTACCCGCCAG 572  
|||||

RESULT 13  
A1681540 402 bp mRNA 1linear EST 16-DEC-1999  
LOCUS A1681540  
DEFINITION tx47e07.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA IMAGE:2272740 3'

similar to TR:076093 076093 FIBROBLAST GROWTH FACTOR 18. ;, mRNA  
Sequence.  
ACCESSION A1681540  
VERSION A1681540.1 GI:4891722  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 402)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution Information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.lnlnl.gov/bdrip/image/image.html  
Insert Length: 526 Std Error: 0.00  
Seq primer: -40UP from Gibco.

FEATURES  
source  
Location/Qualifiers  
1. 402  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="IMAGE:2272740"  
/clone\_1lb="NCI\_CGAP\_Lu24"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: pTZ19-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Lu5 was prepared, and ss circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subclonable hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (clonoids  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 120 a 110 c 95 g 76 t 1 others  
ORIGIN

Query Match 25.5%; Score 401; DB 9; Length 402;  
Best Local Similarity 99.8%; Pred. No. 4.1e-45;  
Matches 401; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1075 AAGCGTACCCCAAGGGGAGCGGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 1134  
|||||

Db 1 AAGCGTACCCCAAGGGGAGCGGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 60  
|||||

QY 1135 AAGAGTCCCGTGGATCCGCGCCACACACCTGCTAGGCGACCCGCGGCGCTTC 1194  
|||||

Db 61 AAGAGTCCCGTGGATCCGCGCGCCACACACCTGCTAGGCGACCCGCGGCGCTTC 120  
|||||

QY 1195 AGGTGCGCTGGCCACACACTCCACGAAACCTCATCAGAGATATTTTACATG 1254  
|||||

Db 121 AGGTGCGCTGGCCACACACTCCACGAAACCTCATCAGAGATATTTTACATG 180  
|||||

QY 1255 AAAAATTAAGGAAGAGCTTATTTTGTACATTTGTTTAAAGAAACAAAACCTGAC 1314  
|||||

Db 181 AAAAATTAAGGAAGAGCTTATTTTGTACATTTGTTTAAAGAAACAAAACCTGAC 240  
|||||

QY 1315 CAAAACCTTTGGGGGAGGGGTGATAGGATTTTATTTGACTTGAACCCCGATGAC 1374  
|||||

Db 241 CAAAACCTTTGGGGGAGGGGTGATAGGATTTTATTTGACTTGAACCCCGATGAC 300  
|||||

QY 1375 AAAAGACTACGCCAAAGGAGCTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACA 1434  
|||||

Db 301 AAAAGACTACGCCAAAGGAGCTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACA 360  
|||||

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OY 1435 GACAACTCTAAACTCGTCCCGACAGAGAGACTTGATGAGA 1476
DB 361 GACAACTCTAAACTCGTCCCGACAGAGAGACTTGATGAGA 402

RESULT 14
LOCUS AI002437 401 bp mRNA linear EST 23-JUL-1998
DEFINITION or78f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1601991 3',
mRNA sequence.
ACCESSION AI002437
VERSION AI002437.1 GI:3202771
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.livnl.gov/bbrp/image/image.html
Insert length: 841 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 394.
FEATURES
Source
Location/Qualifiers
1..401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1601991"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: Lung; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 119 a 110 c 94 g 78 t
ORIGIN
Query Match 25.4%; Score 399.4; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 6.8e-45;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1075 AAGCGCTACCCCAAGGGGAGCGGAGCTTCAGAAAGCCCTTAAGTACACGACGGTGACC 1134
DB 1 AAGCGCTACCCCAAGGGGAGCGGAGCTTCAGAAAGCCCTTAAGTACACGACGGTGACC 60
OY 1135 AAGAGTCCCGTCGGATCCGGCCACACACACCTGCTAGAGCCCGCGCGGCGCCCTC 1194
DB 61 AAGAGTCCCGTCGGATCCGGCCACACACACCTGCTAGAGCCCGCGCGGCGCCCTC 120
OY 1195 AGGTGCGCCCTGGCCACACTCACACTCCAGAAAGCTGCATCAGAGAAATATTTTACATG 1254
DB 121 AGGTGCGCCCTGGCCACACTCACACTCCAGAAAGCTGCATCAGAGAAATATTTTACATG 180
OY 1235 AAAATTAAGGAAGAGCTTATTTTGTATCATTTGTTTAAAGAAGACAAAAGTGAAC 1314

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DB 181 AAAAATAGGAAGAGAGCTCTATTTTGTATCATTTGTTTAAAGAAGACAAAAGTGAAC 240
OY 1315 CAAAACTCTGGGGGAGGGGATGATTAAGATTTTATTTGTTGACTGAAACCCCGATGAC 1374
DB 241 CAAAACTCTGGGGGAGGGGATGATTAAGATTTTATTTGTTGACTGAAACCCCGATGAC 300
OY 1375 AAAAGACTCAGCCAAAGGAGCTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACA 1434
DB 301 AAAAGACTCAGCCAAAGGAGCTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACA 360
OY 1435 GACAACTCTAAACTCGTCCCGACAGAGAGACTTGATGAGG 1475
DB 361 GACAACTCTAAACTCGTCCCGACAGAGAGACTTGATGAGG 401

RESULT 15
LOCUS AI193544 405 bp mRNA linear EST 13-OCT-1998
DEFINITION ge70e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1744344 3', mRNA sequence.
ACCESSION AI193544
VERSION AI193544.1 GI:3744753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 399.
FEATURES
Source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744344"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W. "
BASE COUNT 122 a 107 c 96 g 80 t
ORIGIN
Query Match 25.3%; Score 397; DB 9; Length 405;
Best Local Similarity 98.8%; Pred. No. 1.4e-44;
Matches 400; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1075 AAGCGTACCCCAAGGGGAGCGGAGCTTCAGAAAGCCCTTAAGTACACGAGGTGACC 1134
DB 1 AAGCGTACCCCAAGGGGAGCGGAGCTTCAGAAAGCCCTTAAGTACACGAGGTGACC 60
OY 1135 AAGAGTCCCGTCGGATCCGGCCACACACCTGCTAGAGCCCGCGCGGCGCCCTC 1194
DB 61 AAGAGTCCCGTCGGATCCGGCCACACACCTGCTAGAGCCCGCGCGGCGCCCTC 120

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QY 1195 AGTGGCCCTGGCCACATCAGACTCCCGAGAAAATGATCAGAGAAATATTTTACATG 1254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AGTGGCTCTGGGGGACACTCCAGAAAATGATCAGAGAAATATTTTACATG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1255 AAAAATAGAGAGAGCTCTATTTTGTACATTGTGTTAAAGAGACAAAACTGAAC 1314
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AAAAATAGAGAGAGCTCTATTTTGTACATTGTGTTAAAGAGACAAAACTGAAC 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1315 CAAAACTCTGGGGGAGGGGTGATTAAGATTTTGTGACTTGAACCCCGATGAC 1374
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CAAAACTCTGGGGGAGGGGTGATTAAGATTTTGTGACTTGAACCCCGATGAC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1375 AAAAGACTCAGCAAAAGGACTGTAGTCAACCCACAGGTGCTCTCTCTAGAAC 1434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AAAAGACTCAGCATAGGACTGTAGTCAACCCACAGGTGCTCTCTCTAGAAC 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1435 GACAACTCTAAACTGTCCCGAGAGAGACTTGAATGAGGAAC 1479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GACAACTCTAAACTGTCTCAGAGAGAGACTTGAATGAGGAAC 405
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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